

SEQUENCE LISTING

W/B28

<110> biosyn Arzneimittel GmbH

<120> RECOMBINANT MISTLETOE LECTINS

<130> PCT 980

<140> PCT/EP99/00696

<141> 1999-02-03

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<151> 1998-02-03

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 35 40 45
 Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Gln Gly Xaa Asp
 50 55 60
 Ser Xaa Thr Ala Ala Ile Asp Val Thr Asn Xaa Tyr Val Val Ala Tyr
 65 70 75 80
 Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly Ala
 85 90 95
 Glu Thr His Leu Phe Thr Gly Thr Thr Arg Xaa Ser Ser Leu Pro Phe
 100 105 110
 Xaa Gly Ser Tyr Xaa Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln
 115 120 125
 Ile Pro Leu Gly Ile Xaa Gln Leu Ile Gln Ser Val Xaa Ala Leu Arg
 130 135 140

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Xaa Pro Gly Gly Ser Thr Arg Xaa Gln Ala Arg Ser Ile Leu Ile Leu
 145 150 155 160
 Ile Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg
 165 170 175
 Xaa Arg Gln Xaa Ile Asn Ser Gly Xaa Ser Phe Leu Pro Asp Xaa Tyr
 180 185 190
 Met Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln
 195 200 205
 His Ser Thr Asp Gly Val Phe Asn Asn Pro Xaa Arg Leu Ala Ile Xaa
 210 215 220
 Xaa Gly Asn Phe Val Thr Leu Xaa Asn Val Arg Xaa Val Ile Ala Ser
 225 230 235 240
 Leu Ala Ile Met Leu Phe Val Cys Gly Glu Arg Pro Ser Ser Ser Asp
 245 250 255
 Val Arg Tyr Trp Pro Leu Val Ile Arg Pro Val Ile Ala Asp Asp Val
 260 265 270
 Thr Cys Ser Ala Ser Glu Pro Thr Val Arg Ile Val Gly Arg Xaa Gly
 275 280 285
 Met Xaa Val Asp Val Arg Asp Asp Asp Phe His Asp Gly Asn Gln Ile
 290 295 300
 Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln Leu Trp Thr
 305 310 315 320
 Ile Lys Arg Asp Xaa Thr Ile Arg Ser Asn Gly Ser Cys Leu Thr Thr
 325 330 335
 Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp Cys Asn Thr
 340 345 350
 Ala Val Arg Glu Ala Thr Ile Trp Gln Ile Trp Xaa Asn Gly Thr Ile
 355 360 365
 Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser Gly Ile Lys
 370 375 380
 Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu Gly Gln Gly
 385 390 395 400
 Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr Ile Tyr Gly
 405 410 415
 Phe Arg Asp Leu Cys Met Glu Ser Asn Xaa Gly Ser Val Trp Val Glu
 420 425 430
 Thr Cys Xaa Ser Ser Gln Xaa Asn Gln Xaa Xaa Trp Ala Leu Tyr Gly
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 Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys Leu Thr Xaa
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Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser Cys Ser Xaa
 465 470 475 480
 Xaa Ser Xaa Xaa Gln Arg Trp Val Phe Thr Asn Glu Xaa Ala Ile Leu
 485 490 495
 Asn Leu Lys Xaa Xaa Xaa Xaa Xaa Asp Val Ala Gln Ala Asn Pro Lys
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Phe	Ser	Asn	Glu	Ile	Pro	Leu	Leu	Arg	Gln	Ser	Thr	Ile	Pro	Val	Ser	45
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Asp	Ala	Gln	Arg	Phe	Val	Leu	Val	Glu	Leu	Thr	Asn	Gln	Gly	Xaa	Asp	60
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Ser	Xaa	Thr	Ala	Ala	Ile	Asp	Val	Thr	Asn	Xaa	Tyr	Val	Val	Ala	Tyr	80
65					70				75							
Gln	Ala	Gly	Asp	Gln	Ser	Tyr	Phe	Leu	Arg	Asp	Ala	Pro	Arg	Gly	Ala	95
				85				90								
Glu	Thr	His	Leu	Phe	Thr	Gly	Thr	Thr	Arg	Xaa	Ser	Ser	Leu	Pro	Phe	110
			100					105					110			
Xaa	Gly	Ser	Tyr	Xaa	Asp	Leu	Glu	Arg	Tyr	Ala	Gly	His	Arg	Asp	Gln	125
		115				120						125				
Ile	Pro	Leu	Gly	Ile	Xaa	Gln	Leu	Ile	Gln	Ser	Val	Xaa	Ala	Leu	Arg	140
		130				135					140					
Xaa	Pro	Gly	Gly	Ser	Thr	Arg	Xaa	Gln	Ala	Arg	Ser	Ile	Leu	Ile	Leu	160
145				150				155								
Ile	Gln	Met	Ile	Ser	Glu	Ala	Ala	Arg	Phe	Asn	Pro	Ile	Leu	Trp	Arg	175
				165				170								

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 180 185 190
 Met Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln
 195 200 205
 His Ser Thr Asp Gly Val Phe Asn Asn Pro Xaa Arg Leu Ala Ile Xaa
 210 215 220
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 35 40 45
 Leu Trp Thr Ile Lys Arg Asp Xaa Thr Ile Arg Ser Asn Gly Ser Cys
 50 55 60
 Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
 65 70 75 80
 Cys Asn Thr Ala Val Arg Glu Ala Thr Ile Trp Gln Ile Trp Xaa Asn
 85 90 95
 Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
 100 105 110
 Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
 115 120 125
 Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
 130 135 140
 Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Xaa Gly Ser Val

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145 150 155 160
 Trp Val Glu Thr Cys Xaa Ser Ser Gln Xaa Asn Gln Xaa Xaa Trp Ala
 165 170 175
 Leu Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys
 180 185 190
 Leu Thr Xaa Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser
 195 200 205
 Cys Ser Xaa Xaa Ser Xaa Xaa Gln Arg Trp Val Phe Thr Asn Glu Xaa
 210 215 220
 Ala Ile Leu Asn Leu Lys Xaa Xaa Xaa Xaa Xaa Asp Val Ala Gln Ala
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 35 40 45
 Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Gln Gly Gly Asp
 50 55 60
 Ser Ile Thr Ala Ala Ile Asp Val Thr Asn Leu Tyr Val Val Ala Tyr
 65 70 75 80
 Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly Ala
 85 90 95
 Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe Asn
 100 105 110
 Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln Ile
 115 120 125
 Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg Phe
 130 135 140
 Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu Ile

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145 150 155 160
 Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg Ala
 165 170 175
 Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr Met
 180 185 190
 Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln His
 195 200 205
 Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro Pro
 210 215 220
 Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser Leu
 225 230 235 240
 Ala Ile Met Leu Phe Val Cys Gly Glu Arg Pro Ser Ser Ser Asp Val
 245 250 255
 Arg Tyr Trp Pro Leu Val Ile Arg Pro Val Ile Ala Asp Asp Val Thr
 260 265 270
 Cys Ser Ala Ser Glu Pro Thr Val Arg Ile Val Gly Arg Asn Gly Met
 275 280 285
 Cys Val Asp Val Arg Asp Asp Asp Phe His Asp Gly Asn Gln Ile Gln
 290 295 300
 Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln Leu Trp Thr Ile
 305 310 315 320
 Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys Leu Thr Thr Tyr
 325 330 335
 Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp Cys Asn Thr Ala
 340 345 350
 Val Arg Glu Ala Thr Ile Trp Gln Ile Trp Gly Asn Gly Thr Ile Ile
 355 360 365
 Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser Gly Ile Lys Gly
 370 375 380
 Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu Gly Gln Gly Trp
 385 390 395 400
 Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr Ile Tyr Gly Phe
 405 410 415
 Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val Trp Val Glu Thr
 420 425 430
 Cys Val Ser Ser Gln Gln Asn Gln Arg Trp Ala Leu Tyr Gly Asp Gly
 435 440 445
 Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys Leu Thr Cys Gly Arg
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 Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser Cys Ser Ala Gly Ser

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Tyr Phe Arg Phe Ile Thr Leu Leu Arg Asp Tyr Val Ser Ser Gly Ser
20 25 30
Phe Ser Asn Glu Ile Pro Leu Leu Arg Gln Ser Thr Ile Pro Val Ser
35 40 45

Asp	Ala	Gln	Arg	Phe	Val	Leu	Val	Glu	Leu	Thr	Asn	Gln	Gly	Gln	Asp	50	55	60
Ser	Ile	Thr	Ala	Ala	Ile	Asp	Val	Thr	Asn	Ala	Tyr	Val	Val	Ala	Tyr	65	70	75
Gln	Ala	Gly	Asp	Gln	Ser	Tyr	Phe	Leu	Arg	Asp	Ala	Pro	Arg	Gly	Ala	85	90	95
Glu	Thr	His	Leu	Phe	Thr	Gly	Thr	Thr	Arg	Asp	Arg	Ser	Ser	Leu	Pro	100	105	110
Phe	Thr	Gly	Ser	Tyr	Thr	Asp	Leu	Glu	Arg	Tyr	Ala	Gly	His	Arg	Asp	115	120	125
Gln	Ile	Pro	Leu	Gly	Ile	Glu	Gln	Leu	Ile	Gln	Ser	Val	Ser	Ala	Leu	130	135	140
Arg	Tyr	Pro	Gly	Gly	Ser	Thr	Arg	Ala	Gln	Ala	Arg	Ser	Ile	Leu	Ile	145	150	155
Leu	Ile	Gln	Met	Ile	Ser	Glu	Ala	Ala	Arg	Phe	Asn	Pro	Ile	Leu	Trp	165	170	175
Arg	Tyr	Arg	Gln	Asp	Ile	Asn	Ser	Gly	Glu	Ser	Phe	Leu	Pro	Asp	Met	180	185	190
Tyr	Met	Leu	Glu	Leu	Glu	Thr	Ser	Trp	Gly	Gln	Gln	Ser	Thr	Gln	Val			

195

200

205

Gln His Ser Thr Asp Gly Val Phe Asn Asn Pro Phe Arg Leu Ala Ile
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Ser Thr Gly Asn Phe Val Thr Leu Ser Asn Val Arg Ser Val Ile Ala
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Ser Leu Ala Ile Met Leu Phe Val Cys Gly Glu Arg Pro Ser Ser Ser
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Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
35 40 45

Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
50 55 60

Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
65 70 75 80

Cys Asn Thr Ala Val Arg Glu Ala Thr Ile Trp Gln Ile Trp Gly Asn
85 90 95

Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
100 105 110

Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
115 120 125

Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
130 135 140

Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val
145 150 155 160

Trp Val Glu Thr Cys Val Ser Ser Gln Gln Asn Gln Arg Trp Ala Leu
165 170 175

Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys Leu
180 185 190

Thr Cys Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser Cys
195 200 205

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Ser Ala Gly Ser Ser Gly Gln Arg Trp Val Phe Thr Asn Glu Gly Ala
210 215 220

Ile Leu Asn Leu Lys Asn Gly Leu Ala Met Asp Val Ala Gln Ala Asn
225 230 235 240

Pro Lys Leu Arg Arg Ile Ile Ile Tyr Pro Ala Thr Gly Lys Pro Asn
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Gln Met Trp Leu Pro Val Pro
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Arg Asn Gly Met Arg Val Asp Val Arg Asp Asp Asp Phe His Asp Gly
20 25 30

Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
35 40 45

Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
50 55 60

Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
65 70 75 80

Cys Asn Thr Ala Val Arg Glu Ala Thr Ile Trp Gln Ile Trp Asp Asn
85 90 95

Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
100 105 110

Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
115 120 125

Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
130 135 140

Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val
145 150 155 160

Trp Val Glu Thr Cys Asp Ser Ser Gln Lys Asn Gln Gly Lys Trp Ala
165 170 175

Leu Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys
180 185 190

Leu Thr Ser Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser
195 200 205

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Cys Ser Gly Ala Ser Gly Ser Gln Arg Trp Val Phe Thr Asn Glu Gly
210 215 220

Ala Ile Leu Asn Leu Lys Asn Gly Leu Ala Met Asp Val Ala Gln Ala
225 230 235 240

Asn Pro Lys Leu Arg Arg Ile Ile Ile Tyr Pro Ala Thr Gly Lys Pro
245 250 255

Asn Gln Met Trp Leu Pro Val Phe
260

<210> 8
<211> 264
<212> PRT
<213> Artificial Sequence

<400> 8

Asp Asp Val Thr Cys Ser Ala Ser Glu Pro Thr Val Arg Ile Val Gly
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Arg Ser Gly Met Arg Val Asp Val Arg Asp Asp Asp Phe His Asp Gly
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Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
35 40 45

Leu Trp Thr Ile Lys Arg Asp Asn Thr Ile Arg Ser Asn Gly Ser Cys
50 55 60

Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
65 70 75 80

Cys Asn Thr Ala Val Arg Glu Ala Thr Ile Trp Gln Ile Trp Asp Asn
85 90 95

Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
100 105 110

Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
115 120 125

Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
130 135 140

Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gln Gly Ser Val
145 150 155 160

Trp Val Glu Thr Cys Asp Ser Ser Gln Lys Asn Gln Gly Lys Trp Ala
165 170 175

Leu Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys
180 185 190

Leu Thr Val Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser
195 200 205

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Cys Ser Gly Ala Ser Gly Ser Gln Arg Trp Val Phe Thr Asn Glu Tyr
210 215 220

Ala Ile Leu Asn Leu Lys Ser Gly Leu Ala Met Asp Val Ala Gln Ala
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Asn Pro Lys Leu Arg Arg Ile Ile Ile Tyr Pro Ala Thr Gly Lys Pro
245 250 255

Asn Gln Met Trp Leu Pro Val Phe
260

<210> 9
<211> 264
<212> PRT
<213> Artificial Sequence

<400> 9

Asp Asp Val Thr Cys Ser Ala Ser Glu Pro Thr Val Arg Ile Val Gly
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Arg Asn Gly Met Arg Val Asp Val Arg Asp Asp Asp Phe His Asp Gly
20 25 30

Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
35 40 45

Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
50 55 60

Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
65 70 75 80

Cys Asn Thr Ala Val Arg Glu Ala Thr Ile Trp Gln Ile Trp Asp Asn
85 90 95

Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
100 105 110

Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
115 120 125

Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
130 135 140

Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val
145 150 155 160

Trp Val Glu Thr Cys Asp Ser Ser Gln Lys Asn Gln Gly Lys Trp Ala
165 170 175

Leu Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys
180 185 190

Leu Thr Ser Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser
195 200 205

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Cys Ser Gly Ala Ser Gly Ser Gln Arg Trp Val Phe Thr Asn Glu Gly
210 215 220

Ala Ile Leu Asn Leu Lys Thr Gly Leu Ala Met Asp Val Ala Gln Ala
225 230 235 240

Asn Pro Lys Leu Arg Arg Ile Ile Ile Tyr Pro Ala Thr Gly Lys Pro
245 250 255

Asn Gln Met Trp Leu Pro Val Phe
260

<210> 10
<211> 264
<212> PRT
<213> Artificial Sequence

<400> 10

Asp Asp Val Thr Cys Ser Ala Ser Glu Pro Thr Val Arg Ile Val Gly
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Arg Asn Gly Met Arg Val Asp Val Arg Asp Asp Asp Phe His Asp Gly
20 25 30

Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
35 40 45

Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
50 55 60

Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
65 70 75 80

Cys Asn Thr Ala Val Arg Glu Ala Thr Ile Trp Gln Ile Trp Asp Asn
85 90 95

Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
100 105 110

Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
115 120 125

Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
130 135 140

Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val
145 150 155 160

Trp Val Glu Thr Cys Asp Ser Ser Gln Lys Asn Gln Gly Lys Trp Ala
165 170 175

Leu Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys
180 185 190

Leu Thr Ser Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser
195 200 205

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21-37

Cys Ser Gly Ala Ser Gly Ser Gln Arg Trp Val Phe Thr Asn Glu Gly
 210 215 220
 Ala Ile Leu Asn Leu Lys Lys Gly Pro Ala Met Asp Val Ala Gln Ala
 225 230 235 240
 Asn Pro Lys Leu Arg Arg Ile Ile Ile Tyr Pro Ala Thr Gly Lys Pro
 245 250 255
 Asn Gln Met Trp Leu Pro Val Phe
 260

<210> 11
 <211> 264
 <212> PRT
 <213> Artificial Sequence

<400> 11

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 Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
 35 40 45
 Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
 50 55 60
 Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
 65 70 75 80
 Cys Asn Thr Ala Val Arg Glu Ala Thr Ile Trp Gln Ile Trp Asp Asn
 85 90 95
 Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
 100 105 110
 Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
 115 120 125
 Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
 130 135 140
 Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val
 145 150 155 160
 Trp Val Glu Thr Cys Asp Ser Ser Gln Lys Asn Gln Gly Lys Trp Ala
 165 170 175
 Leu Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys
 180 185 190
 Leu Thr Ser Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser
 195 200 205

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Cys Ser Gly Ala Ser Gly Ser Gln Arg Trp Val Phe Thr Asn Glu Gly
 210 215 220
 Ala Ile Leu Asn Leu Lys Asn Ser Leu Met Val Asp Val Ala Gln Ala
 225 230 235 240
 Asn Pro Lys Leu Arg Arg Ile Ile Ile Tyr Pro Ala Thr Gly Lys Pro
 245 250 255
 Asn Gln Met Trp Leu Pro Val Phe
 260

<210> 12
 <211> 1598
 <212> DNA
 <213> Artificial Sequence

<220>
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 <222> 319
 <223> product= "n is gat aga or missing"
 /label= Z1

<220>
 <221> misc_feature
 <222> 1322
 <223> product= "n is ggc or missing"
 /label= Z2

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 cgtcagtcta cgatccccgt ctccgatgcg caaagatttg tcttggtgga gctcaccaac 180
 caggggsrrg actcgrtyac ggccgccatc gacgttacca atsyktacgt cgtggcttac 240
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anaratgggc tttgtacggg gatggttcta tacgccccaa acaaaaacca gaccaatgcc 1380
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<210> 13
<211> 763
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> 319
<223> product= "n is gat aga or missing"
/label= z1

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cgtcagtcta cgatccccgt ctccgatgcg caaagatttg tcttgggtgga gctcaccaac 180
caggggsrrg actcgrtyac ggccgccatc gacgttacca atsyktaagt cgtggcttac 240
caagcaggcg accaatccta ctttttgcgc gacgcaccac gcggcgcgga aacgcacctc 300
ttcaccggca ccaccgant cctctctccc attcamygga agctacmcyg atctggagcg 360
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 taacagtggg gmrtcatttc tgccagacrt gtacatgctg gagctggaga cgagttgggg 600
 ccaacaatcc acgcaagtcc agcattcaac cgatggcggt tttaataacc cawtycggtt 660
 ggctataycy mcyggtaact tcgtgacgtt gwcyaatgtt cgckmygtga tcgccagctt 720
 ggcgatcatg ttgtttgtat gcggagagcg gccatcttcc tct 763

<210> 14
 <211> 793
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> 517
 <223> product= "n is ggc or missing"
 /label= Z2

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 aagtccaaca atgatccgaa tcagttgtgg acgatcaaaa gggatrrmac cattogatcc 180
 aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac 240
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 aatccaagat ccaatctggt tttggcagca tcactctgaa tcaaaggcac tacgcttacg 360
 gtgcaaacac tggattacac gttgggacag ggctggcttg ccggtaatga taccgcccc 420
 cgcgaggtga ccatatatgg tttcagggac ctttgcattg aatcaaatsr agggagtgtg 480
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 caatgaakrs gccattttga atttaaagav wrgsyygrys rtggatgtgg cgcaagcaaa 720
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 tcccgtgyym tga 793

<210> 15
 <211> 1596

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<212> DNA
<213> Artificial Sequence

<400> 15

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cgtcagtcta cgatccccgt ctccgatgcg caaagatttg tcttggtgga gctcaccaac	180
caggggggag actcgatcac ggccgcatc gacgttacca atctgtacgt cgtggcttac	240
caagcaggcg accaatccta ctttttgcg gacgcaccac gcggcgcgga aacgcacctc	300
ttcaccggca ccaccgatc ctctctcca ttcaacggaa gctaccctga tctggagcga	360
tacgccggac atagggacca gatccctctc ggtatagacc aactcattca atccgtcacg	420
gcgcttcggt ttccggggcg cagcacgcgt acccaagctc gtctgatttt aatcctcatt	480
cagatgatct ccgaggccgc cagattcaat cccatcttat ggagggtcg ccaatacatt	540
aacagtgggg cgctatttct gccagacgtg tacatgctgg agctggagac gagttggggc	600
caacaatcca cgcaagtcca gcattcaacc gatggcggtt ttaataaacc aattcggttg	660
gctatacccc ccggttaact cgtgacgttg aaccaatgtc gcgacgtgat cgccagcttg	720
gcgateatgt tgtttgatg cggagagcgg ccatcttcct ctgacgtgcg ctattggccg	780
ctggtcatac gaccctgat agccgatgat gttacctgca gtgcttcgga acctacggtg	840
cggattgtgg gtcgaaatgg catgtgcgtg gacgtccgag atgacgattt ccacgatggg	900
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tctgggcagc gatgggtgtt taccaatgaa ggggccattt tgaatttaaa gaatgggttg	1500
gccatggatg tggcgcaagc aaatccaaag ctccgccgaa taattatcta tcctgccaca	1560
ggaaaaccaa atcaaattg gttcccggtg ccatga	1596

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<210> 16
 <211> 762
 <212> DNA
 <213> Artificial Sequence

<400> 16
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 cgtcagtcta cgatccccgt ctccgatgcg caaagatttg tcttggtgga gctcaccaac 180
 caggggcagg actcggttac ggccgccatc gacgttacca atgcttacgt cgtggcttac 240
 caagcaggcg accaatccta ctttttgcg gacgcaccac gcggcgcgga aacgcacctc 300
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 tacgccggac atagggacca gatccctctc ggtatagacc aactcattca atccgtcacg 420
 gcgcttcggt ttccgggagg cagcacgctg acccaagctc gttcgatttt aatcctcatt 480
 cagatgatct ccgaggccgc cagattcaat cccatcttat ggaggtaccg ccaatacatt 540
 aacagtgggg cgtcattttc gccagacgtg tacatgctgg agctggagac gagttggggc 600
 caacaatcca cgcaagtcca gcattcaacc gatggcggtt ttaataaccc aattcggttg 660
 gctatacccc ccggttaactt cgtgacgttg accaatgttc gcaagtgat cgcagcttg 720
 gcgatcatgt tgtttgtatg cggagagcgg ccatcttctt ct 762

<210> 17
 <211> 768
 <212> DNA
 <213> Artificial Sequence

<400> 17
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 cgtcagtcta cgatccccgt ctccgatgcg caaagatttg tcttggtgga gctcaccaac 180
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 ttcaccggca ccacccgaga tagatcctct ctccattca ctggaagcta caccgatctg 360
 gagcgatacg ccggacatag ggaccagatc cctctcggtg tagagcaact cattcaatcc 420
 gtctctgcgc ttcgttacct gggcggcagc acgcgtgctc aagctcggtc gattttaatc 480

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ctcattcaga tgatctccga ggccgccaga ttcaatccca tcttatggag gtaccgcaa 540
gatattaaca gtggggaatc atttctgcca gacatgtaca tgctggagct ggagacgagt 600
tggggccaaac aatccacgca agtcacagcat tcaaccgatg gcgtttttaa taaccattc 660
cggttggcta tatctactgg taacttcgtg acgttgctta atgttcgctc tgtgatcgcc 720
agcttggcga tcatgttggt tgtatgcgga gagcgccat cttcctct 768

<210> 18
<211> 1596
<212> DNA
<213> Artificial Sequence

<400> 18
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agacaatcta ctattccagt ttctgatgct cagcgtttcg ttcttggtga attgactaac 180
caaggaggtg atagtattac tgctgctatt gatgtgacta acctttatgt tgttgcatat 240
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tttactggta caacacggag ttctttgcct tttacgggtt cttatccaga cttggaaaga 360
tatgctggtc acagagatca aattccattg ggaattgac agttgatcca gagtgttact 420
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caaatgatta gtgaagctgc taggtttaac cctattcttt ggagagcaag acagtatatc 540
aactctggtg cttctttcct tcctgatggt tatatgcttg aacttgaaac ttcattggga 600
cagcagtcta ctcagggtca acacagtaca gacggtgtgt tcaacaatcc tatcagactt 660
gcaattccac ctggaaattt tgttactctt acaaactgga gagatgttat tgcttctctt 720
gctattatgc ttttcgtttg tggtgaaaga ccttctagtt ctgatgttag atactggcca 780
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ggtattaagg gaacaacttt gactgttcag actttggact atactcttgg tcaaggatgg 1200
ttggctggaa acgacacagc tcctagagaa gttacaatct acggatttag agatttgtgt 1260

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atggagtcta acggtggatc tgtttggggt gaaacttggtg tttcatctca gcaaaatcag 1320
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<210> 19
 <211> 762
 <212> DNA
 <213> Artificial Sequence

<400> 19
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 agacaatcta ctattccagt ttctgatgct cagcgtttcg ttcttggtga attgactaac 180
 caaggacagg atagtgttac tgctgctatt gatgtgacta acgcttatgt tgttgcatat 240
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 tttactggta caacacggag ttctttgcct tttaaagggtt cttatccaga cttggaaaga 360
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 gctttgagat tcccagggtg atctactaga acacaggcaa gatctatcct tattttgatc 480
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 cagcagtcta ctcagggtca acacagtaca gacgggtgtg tcaacaatcc tatcagactt 660
 gcaattccac ctggaaattt tgttactctt acaaacgtga gagatgttat tgcttctctt 720
 gctattatgc ttttcgtttg tggtgaaaga ccttctagtt ct 762

<210> 20
 <211> 768
 <212> DNA
 <213> Artificial Sequence

<400> 20
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 caggctggtg atcagtctta tttccttagg gatgctccta gaggagctga gactcatttg 300
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 agacttgcaa tttctactgg aaattttggt actctttcta acgtgagatc tgttattgct 720
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<210> 21
 <211> 792
 <212> DNA
 <213> Artificial Sequence

<400> 21

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 aagtccaaca atgatccgaa tcagttgtgg acgatcaaaa gggatggaac cattcgatcc 180
 aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac 240
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 aatccaagat ccaatctggt tttggcagca tcatctggaa tcaaaggcac tacgcttacg 360
 gtgcaaacac tggattacac gttgggacag ggctggcttg ccggtaatga taccgcccc 420
 cgcgagggtga ccatatatgg tttcagggac ctttgcattg aatcaaattg agggagtgtg 480
 tgggtggaga cgtgcgtgag tagccaacag aaccaaagat gggctttgta cggggatggt 540
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 aatgaagggg ccattttgaa tttaaagaat gggttggcca tggatgtggc gcaagcaa 720
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<210> 22
 <211> 795
 <212> DNA
 <213> Artificial Sequence

<400> 22

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aagtccaaca atgatccgaa tcagttgtgg acgatcaaaa gggatggaac cattcgatcc      180
aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac      240
tgtaatactg ctgtgcggga ggccactatt tggcagatat gggacaatgg gaccatcatc      300
aatccaagat ccaatctggt tttggcagca tcatctggaa tcaaaggcac tacgcttacg      360
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cgcgaggtga ccatatatgg tttcagggac ctttgcattg aatcaaattg agggagtgtg      480
tgggtggaga cgtgcgacag tagccaaaag aaccaaggca aatgggcttt gtacggggat      540
ggttctatac gcccacaaca aaaccaagac caatgcctca cctctgggag agactccggt      600
tcaacagtaa tcaatatagt tagctgcagc ggagcttcgg ggtctcagcg atgggtgttt      660
accaatgaag gggccatttt gaatttaaag aatgggttgg ccatggatgt ggegeaagca      720
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<210> 23
 <211> 795
 <212> DNA
 <213> Artificial Sequence

<400> 23

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aagtccaaca atgatccgaa tcagttgtgg acgatcaaaa gggataaac cattcgatcc      180
aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac      240
tgtaatactg ctgtgcggga ggccactatt tggcagatat gggacaatgg gaccatcatc      300
aatccaagat ccaatctggt tttggcagca tcatctggaa tcaaaggcac tacgcttacg      360
gtgcaaacac tggattacac gttgggacag ggctggcttg ccggtaatga taccgccccca      420
  
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 ggttctatac gcccacaaaca aaaccaagac caatgcctca cgttgggag agactccgtt 600
 tcaacagtaa tcaatatagt tagctgcagc ggagcttcgg ggtctcagcg atgggtgttt 660
 accaatgaat acgccatttt gaatttaaag agtgggttgg ccatggatgt ggcgcaagca 720
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 <213> Artificial Sequence

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 aagtccaaca atgatccgaa tcagttgtgg acgatcaaaa gggatggaac cattcgatcc 180
 aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac 240
 tgtaatactg ctgtgcggga ggccactatt tggcagatat gggacaatgg gaccatcacc 300
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 accaatgaag gggccatttt gaatttaaag actgggttgg ccatggatgt ggcgcaagca 720
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<210> 25
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 <212> DNA
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<400> 25

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 aagtccaaca atgatccgaa tcagttgtgg acgatcaaaa gggatggaac cattcgatcc 180
 aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac 240
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 aatccaagat ccaatctggt tttggcagca tcactctgga tcaaaggcac tacgcttacg 360
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 cgcgaggtga ccatatatgg tttcaggac ctttgcattg aatcaaatgg agggagtgtg 480
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<210> 26
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 aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac 240
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 tcaacagtaa tcaatatagt tagctgcagc ggagcttcgg ggtctcagcg atgggtgttt 660
 accaatgaag gggccatttt gaatttaaag aatagcttga tgggtgatgt ggcgcaagca 720

00601667 100600

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cttcccgtgt tctga 795

<210> 27
<211> 792
<212> DNA
<213> Artificial Sequence

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aagtctaata acgacccaaa ccaactttgg actattaaga gagacggtac aatcaggtct 180
aacggatctt gtcttactac atacggttac actgcaggag tttacgttat gatttttgat 240
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aacgaggggtg ctatccttaa cttgaagaac ggtcttgcta tggatgttgc tcaggctaac 720
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<210> 28
<211> 795
<212> DNA
<213> Artificial Sequence

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aagtctaata acgacccaaa ccaactttgg actattaaga gagacggtac aatcaggtct 180
aacggatctt gtcttactac atacggttac actgcaggag tttacgttat gatttttgat 240
tgcaacacag cagttagaga agctacaatc tggcaaatct gggataacgg aactattatt 300

09501567 100500

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 tctactgtta ttaacattgt gtcttgttct ggagctagtg gatctcaaag gtgggttttc 660
 acaaacgagg gtgctatcct taacttgaag aacgggtctg ctatggatgt tgctcaggct 720
 aaccctaagt tgagaaggat tatcatttac ccagctactg gtaagcctaa ccagatgtgg 780
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<210> 29
 <211> 795
 <212> DNA
 <213> Artificial Sequence

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 aagtctaata acgacccaaa ccaactttgg actattaaga gagacaatac aatcaggctc 180
 aacggatctt gtcttactac atacgggtac actgcaggag tttacgttat gatttttgat 240
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 acaaacgagt atgctatcct taacttgaag tccgggtctg ctatggatgt tgctcaggct 720
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 <212> DNA

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<213> Artificial Sequence

<400> 30

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<210> 31
 <211> 795
 <212> DNA
 <213> Artificial Sequence

<400> 31

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 aagtctaata acgacccaaa ccaactttgg actattaaga gagacggtac aatcagggtct 180
 aacggatctt gtcttactac atacggttac actgcaggag tttacgttat gatttttgat 240
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 gttcagactt tggactatac tcttgggtcaa ggatgggttg ctggaaacga cacagctcct 420
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<210> 32
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 aagtctaata acgacccaaa ccaactttgg actattaaga gagacggtac aatcaggctc 180
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<210> 33
 <211> 20
 <212> DNA
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<400> 33
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<210> 34

09601667 100600

<211> 20
<212> DNA
<213> Artificial Sequence

<400> 34

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20

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<400> 35

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<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<400> 36

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24

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